PATENT

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re patent application of

Zhongyi LI *et al.*	Group Art Unit: 1638
Serial No. 09/508,377	Examiner: Stuart Baum
Filed: June 9, 2000	Attorney Docket No: 017227-0195

For: ***REGULATION OF GENE EXPRESSION IN PLANTS***

DECLARATION UNDER 37 C.F.R. § 1.132

I, Sadequr Rahman, declare:

1. That my professional training and experience are documented in the abridged *curriculum vitae* that is attached as Exhibit 1. I have a Ph.D. in Biochemistry from the University of London, UK, awarded in 1983. My Ph.D. dissertation is titled "The synthesis of seed storage proteins in barley."

2. I am employed now as a Principal Research Scientist by the Commonwealth Scientific and Industrial Research Organization, which is located in Canberra, Australian Capital Territory, Australia. My employment history is documented in Exhibit 1. I have researched starch biosynthesis for the past twelve years.

3. I am named as an inventor in the above-captioned application ("the application").

4. I have considered and believe that I understand the Examiner Telephone Interview of February 10, 2004, the Advisory Action of December 17, 2003, the specification of the application, and pending claims 48-68.

5. The aforementioned Advisory Action does not address what I understand to be the PTO's standard for "hybridization language." During a February 10th telephone interview, however, the examiner indicated, I am told, that the pending claims do not meet that standard.

6. In relevant part, claim 48 recites "a nucleotide sequence which hybridizes to the *SBE II-D1* gene having the nucleotide sequence shown in SEQ ID NO: 10." According to the examiner, I understand, the recitation of a genus encompassing "a nucleotide sequence which hybridizes to SEQ ID NO: X" requires several specific examples of nucleotide sequences that so hybridize.

7. The application provides at least two examples of nucleotide sequences that hybridize to the *SBE II-D1* gene:
   (A) Example 13 (page 36) details isolation of a *SBE II* gene, represented by clone SBE-9, that encodes the amino acid sequence of SEQ ID NO:12. A cDNA clone having about 97% sequence identity with the coding region

of SEQ ID NO:10, SBE-9 was shown to have SBE activity by Rahman *et al.* (2001), where the clone is designated cDNA1. Exhibit 2 is a copy of latter publication.

(B) Example 14 (page 37) states "sequencing of the SBE II gene contained in clone 2, termed *SBE II-D1* (see SEQ ID NO: 10), showed that it coded for the N-terminal sequence of the major isoform of SBE II expressed in the wheat endosperm, as identified by Morell *et al.* (1997). This is shown in Figure 13." A copy of Morell *et al.* (1997) is attached as Exhibit 3.

8. Based on the examples in the application, a person knowledgeable in plant molecular biology would have understood that the *SBE II-D1* gene (SEQ ID NO:10) codes for the functional starch branching enzyme described by Morell *et al.* (1997), and that the SBE-9 clone (SEQ ID NO:12) is closely related in sequence to the *SBE II-D1* gene.

9. In addition to the examples of the application, I or others working under my supervision have isolated other nucleotide sequences from wheat, coding for starch branching-enzyme II activity, that hybridize to the *SBE II-D1* gene according to the teaching of the application. Using the SBE-9 gene as a probe, we have identified ten cDNA sequences from a wheat library (variety Rosella), all of which hybridize to the *SBE II-D1* gene under stringency conditions similar to those detailed in the examples mentioned in paragraph 7, above. The ten cDNA clones each contained in the range 2000-2500 nucleotides of wheat cDNA, corresponding to the majority of the coding region to near full-length cDNAs for wheat SBE II. Sequence analysis showed that all ten clones contained cDNA sequences that were at least 97% identical to the coding region of the *SBE II-D1* gene (SEQ ID NO:10) and that all ten clones were in the same size class with respect to translation as SBE-9. Furthermore, we similarly constructed a cDNA library from wheat variety Wyuna and isolated at least two cDNA clones encoding SBE activity by hybridisation to an SBE-9 probe. By nucleotide sequence analysis, two of the clones were shown to encode proteins having the same N-terminus as the functional SBE II enzyme reported by Morell *et al.* (1997). Although these two clones were not sequenced in their entirety, I believe that they represent cDNAs encoding functional SBE II enzymes, based on the close similarity of the sequenced regions to the *SBE II-D1* gene and the identity of the obtained amino acid sequences to the corresponding regions of functional SBE II from wheat.

10. I declare that all statements made herein on my knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that wilful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code and that such wilful false statements may jeopardise the validity of the application or any patent issuing thereon.

12.03.04.
Date

Sadequr Rahman
Sadequr Rahman

CURRICULUM VITAE

Name: Sadequr Rahman.

Date/Place of Birth: 7.9.57.

Nationality: Australian/Bangladeshi.

Academic Record

1979	B.A., University of Cambridge, UK. Major in Biochemistry.
1983	Ph.D., University of London, UK. Thesis entitled: "The synthesis of seed storage proteins in barley"
1983-85	MRC Post-doctoral fellow with Prof. Byron G. Lane, Department of Biochemistry, University of Toronto, Canada. Research focus The molecular characterisation of Germin.

Employment Record:

1986	Appointed Assistant Professor, Department of Biochemistry, University of Dhaka, Bangladesh. Research work was concerned with protein breakdown in germinating rice seeds and molecular analysis of *Shigella.*, a common cause of gastro-intestinal disease in Bangaldesh.
1988	Appointed Research Scientist, CSIRO Wheat Research Unit, North Ryde. -Research area. Characterisation of grain softness protein.
1990	Appointed Senior Research Scientist.
1992	Transferred to Canberra to initiate work on starch biosynthesis.
1994	Department of Science, Industry and Trade fellowship to spend three months in Dr. Peter Shewry's laboratory to initiate immuno-screening of expression libraries.
2000	Science and Technology Fellowship, Japan to spend six weeks on transforming rice with wheat large insert clone for isoamylase in Dr. Yasunori Nakamura's laboratory.
2000	Japan Society for the Promotion of Science fellowship to spend eight weeks on detecting wheat genes in rice and wheat by fluorescent in situ hybridisation in Prof. Yasuhiko Mukai's laboratory.
2000	Appointed Principal Research Scientist and Sub-Program Leader, supervising about 20 staff.

Invited Speaker at National and International Symposia (1985 -):

1998	4th Asia Pacfic Conference on Agricultural Biotechnology. Darwin. Chairman of session on Starch.
1998	9th NIAR/COE International Symposium. Tokyo. 'Frontier Research of Plant Genome Functions. ' The structure of genes involved in starch biosynthesis in wheat.'
2001	American Association of Cereal Chemists. (Could not attend).
2002.	Combio Conference, Sydney.

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S.RAHMAN

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